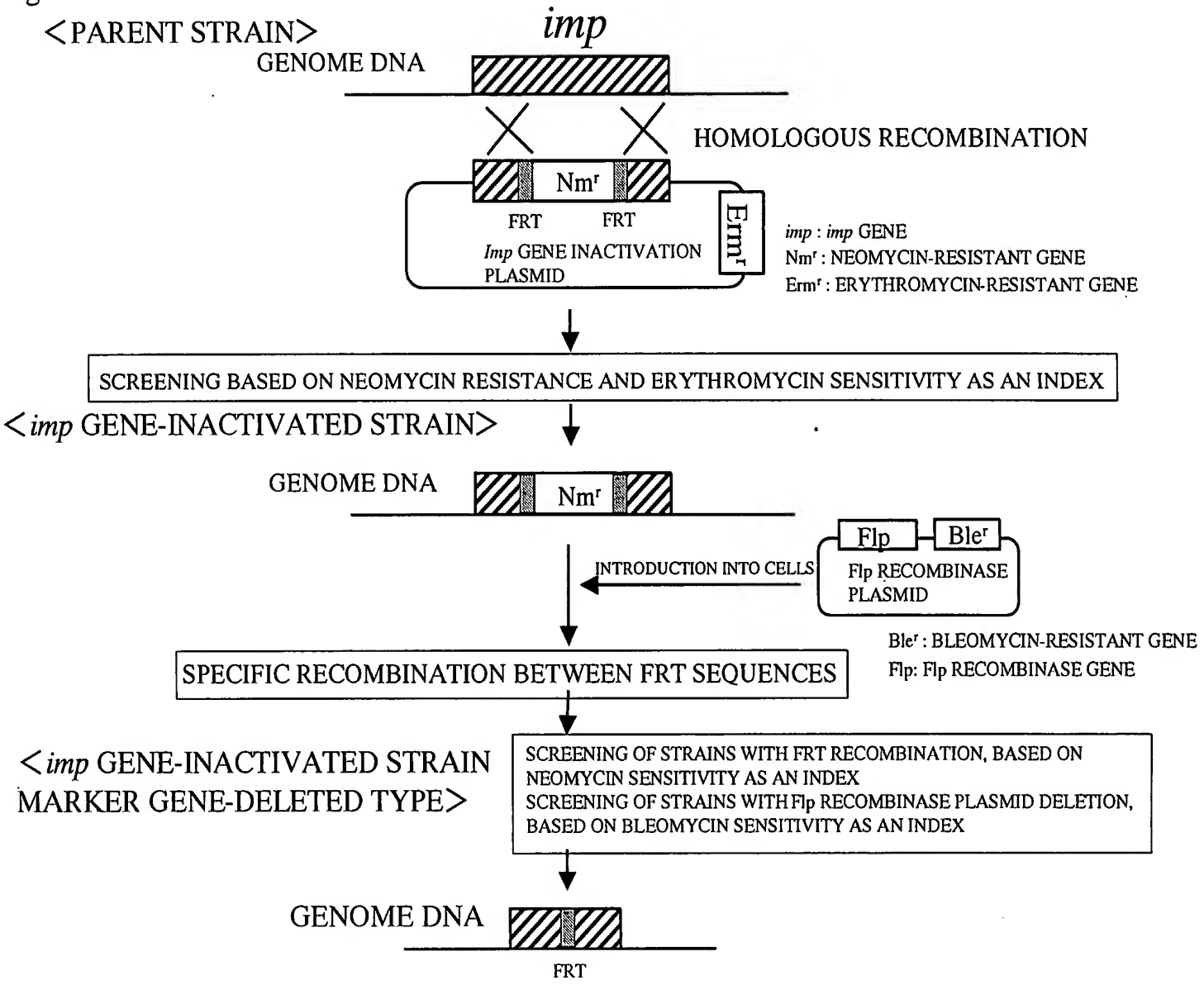
Fig.1



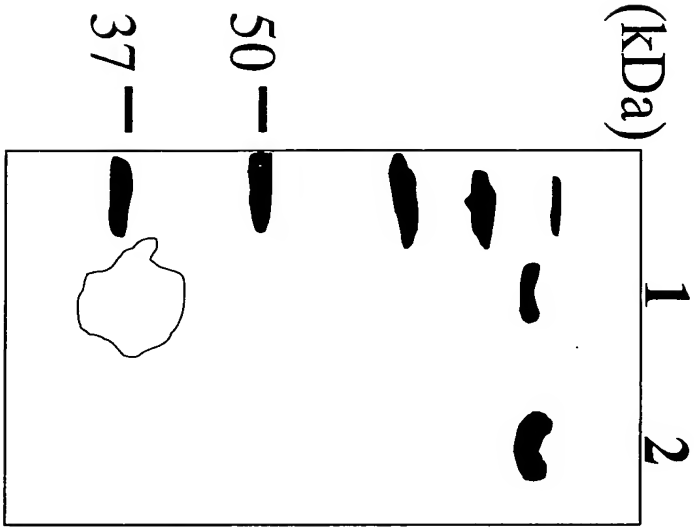



Fig. 2

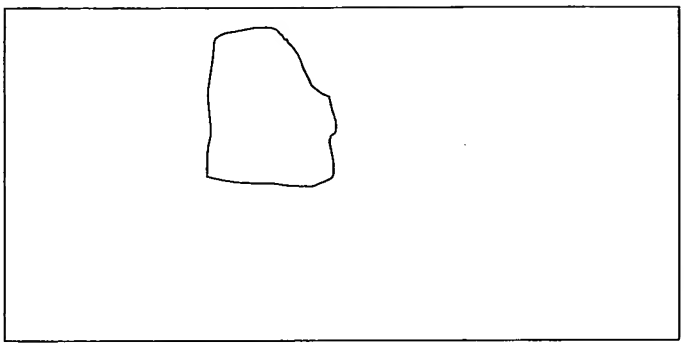


Fig. 3

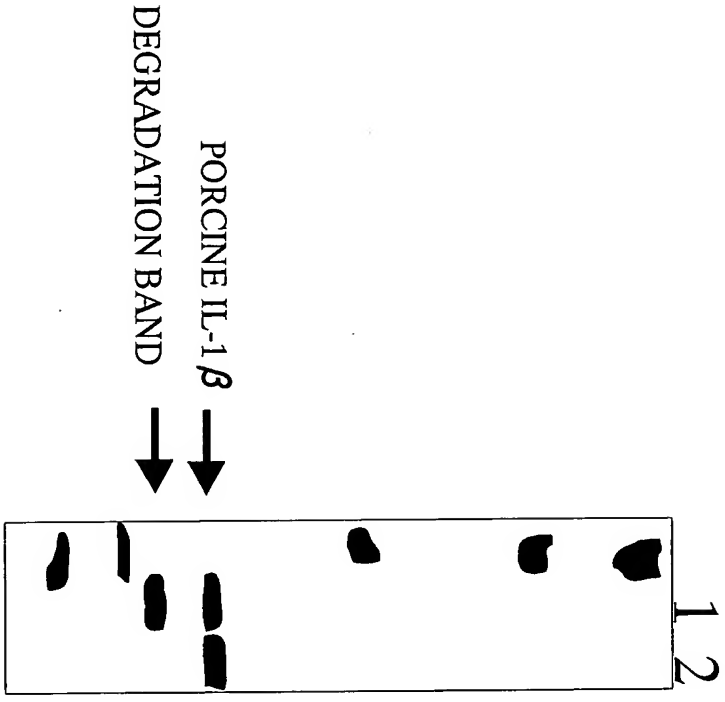



Fig. 4

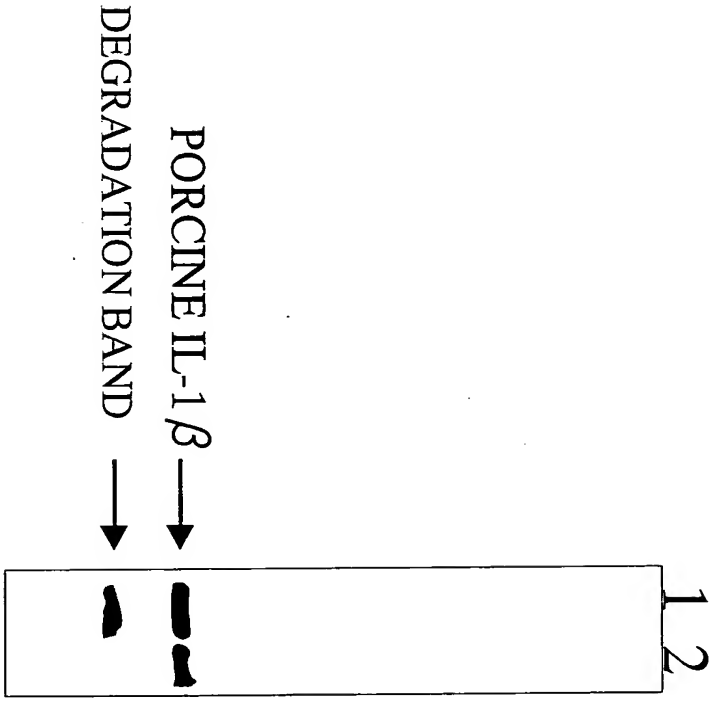



Fig. 5

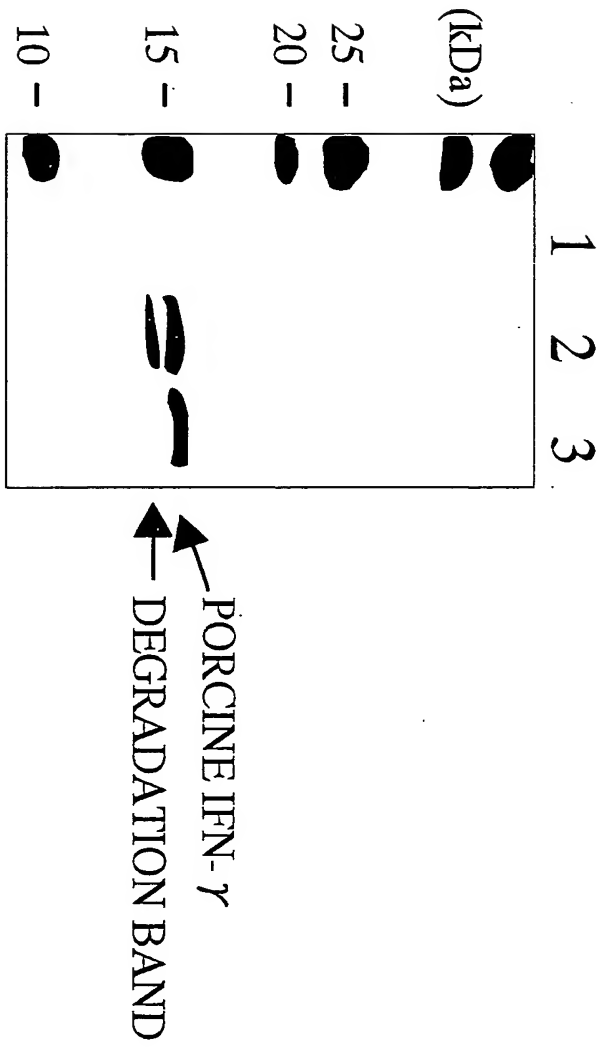



Fig. 6

Fig. 7

hos

```
1   ATGGGTGCCGATATCAAAAATGCGAGTCAACCATTTCTGACCAATGACCAAGTGAAAGAT   60
    MetGlyAlaAspIleLysAsnAlaSerGlnProPheLeuThrAsnAspGlnValLysAsp

61  TTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT  120
    LeuIleAlaLysSerGlnAlaGlyAspThrAspAlaArgGluLeuLeuValAsnSerAsn

121 ATCAGACTGGTCTGGTCCGTCGTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGAT  180
    IleArgLeuValTrpSerValValGlnArgPheIleAsnArgGlyTyrGluAlaAspAsp

181 TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCCGTTGACAAGTTCGATCTTTCGTAC  240
    LeuPheGlnIleGlyCysIleGlyLeuLeuLysAlaValAspLysPheAspLeuSerTyr

241 GATGTGAGATTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTTG  300
    AspValArgPheSerThrTyrAlaValProMetIleIleGlyGluIleGlnArgPheLeu

301 CGCGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG  360
    ArgAspAspGlyThrValLysValSerArgSerLeuLysGluThrAlaAsnLysValArg

361 CGATCAAAGGATGAATTGTACAAGCAATTCGGCCGTGCCCCCACGATCGCAGAAGTGGCA  420
    ArgSerLysAspGluLeuTyrLysGlnPheGlyArgAlaProThrIleAlaGluValAla

421 GAAGCAGTGGGAATCACGCCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCT  480
    GluAlaValGlyIleThrProGluGluValValPheAlaGlnGluAlaSerArgAlaPro

481 TCCTCCATCCATGAGACCGTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAG  540
    SerSerIleHisGluThrValPheGluAsnAspGlyAspProIleThrLeuIleAspGln

541 ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGC  600
    IleAlaAspGluGlyValAsnLysTrpPheGluLysIleAlaLeuLysAspAlaIleSer

601 AGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG  660
    ArgLeuSerGluArgGluGlnLeuIleValTyrLeuArgTyrTyrLysAspGlnThrGln

661 TCTGAGGTAGCAGAGCGTCTAGGGATTTCGCAGGTCCAGGTCTCGCGTCTGGAAAAGCGT  720
    SerGluValAlaGluArgLeuGlyIleSerGlnValGlnValSerArgLeuGluLysArg
```

Fig. 8

```
721  ATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG  756
     IleLeuLeuThrIleLysGluGlnIleGluHis***
```

Fig. 9

emp

```
   1  GTGAACGCAGTGAAGAAAGGCAAGAAGCTATTATCCATCCTATTTTCTTCCTCACTGGTC   60
      ValAsnAlaValLysLysGlyLysLysLeuLeuSerIleLeuPheSerSerSerLeuVal

  61  CTGAGCGGCATTGCGGCGGTTCCAGCGACAGGGATGGCCAAGTCAAAGGACAAGCCGCCG  120
      LeuSerGlyIleAlaAlaValProAlaThrGlyMetAlaLysSerLysAspLysProPro

 121  CTTGAAGTGGATTTGTCCACAGTGAACATGGATCGTTTGGTTAAAGCCTTGATCGACCAA  180
      LeuGluValAspLeuSerThrValAsnMetAspArgLeuValLysAlaLeuIleAspGln

 181  GGTGAAATCGACGAGGACGCCGACCAGGAAGAGATCAACAAAGCTGTGGAGAAGTTTTTG  240
      GlyGluIleAspGluAspAlaAspGlnGluGluIleAsnLysAlaValGluLysPheLeu

 241  AGAGACAAGAAAGTTCCCCACGGCATTGATGACTCCAGCTCCTTCGGGAAAAAAGCAAGC  300
      ArgAspLysLysValProHisGlyIleAspAspSerSerSerPheGlyLysLysAlaSer

 301  AAAACCCAGCTTTCGGCAGTATCAAAGGCAGCAAGCAAAGTATCCAAGCTCAAAGATGAC  360
      LysThrGlnLeuSerAlaValSerLysAlaAlaSerLysValSerLysLeuLysAspAsp

 361  AAGCAAGTGCGCGCTTCCAAGCGGGTACATACGGATAATCTGGTGATTGCCCTGGTCGAG  420
      LysGlnValArgAlaSerLysArgValHisThrAspAsnLeuValIleAlaLeuValGlu

 421  TTCAATGATCTGGAGCACAACCAGGTGCCAAAACAAAGCGATTCCTTGTGGACGGCAGAC  480
      PheAsnAspLeuGluHisAsnGlnValProLysGlnSerAspSerLeuTrpThrAlaAsp

 481  TTCGACCAAAAGCACTACGAGGAAATGCTGTTCGATCGTAAAGGCTATACGACTCCTGAA  540
      PheAspGlnLysHisTyrGluGluMetLeuPheAspArgLysGlyTyrThrThrProGlu

 541  GGGATAAGCATGACCACGATGGCCAAGTACTACTACGAGCAATCGGGTGAGACATGGACC  600
      GlyIleSerMetThrThrMetAlaLysTyrTyrTyrGluGlnSerGlyGluThrTrpThr

 601  GTGGATGGGGTTGTCACTCCGTGGTTGACTGCCGAAAAAGATAAGAAATTCTACGGTGGA  660
      ValAspGlyValValThrProTrpLeuThrAlaGluLysAspLysLysPheTyrGlyGly

 661  AACGATGAAAACGGCAACGATGCCAACCCACGCGATCTGGTCGTCGAGACACTGGAATCT  720
      AsnAspGluAsnGlyAsnAspAlaAsnProArgAspLeuValValGluThrLeuGluSer

 721  GTAGGGGATGCCATCAAGGGTCATGAAGAAGAATACGACCAACGCGACCCGTATGACTTG  780
      ValGlyAspAlaIleLysGlyHisGluGluGluTyrAspGlnArgAspProTyrAspLeu

 781  GATGGAGACAGCGATCTGATGGAGCCGGATGGCATGCTGGACAACCTGATGCTGGTTCAC  840
      AspGlyAspSerAspLeuMetGluProAspGlyMetLeuAspAsnLeuMetLeuValHis
```

Fig. 10

```
841  TCCGGTATTGGTGAAGAGACTGGGGAAGATGCGGATGCGATCTGGTCTCACCGCTGGACT  900
     SerGlyIleGlyGluGluThrGlyGluAspAlaAspAlaIleTrpSerHisArgTrpThr

901  CTGAAAAAGCCGACAGAAATTCCAGGCACCAGCCTGAAAGCTTACGACTACATGATTCAG  960
     LeuLysLysProThrGluIleProGlyThrSerLeuLysAlaTyrAspTyrMetIleGln

961  CCTGAAGATGGCGCACCCGGCGTATTCGCACATGAATACGGACACAACCTGGGACTGCCA 1020
     ProGluAspGlyAlaProGlyValPheAlaHisGluTyrGlyHisAsnLeuGlyLeuPro

1021 GATCTGTATGACACGACAAGACTGGGACATGATTCGCCGGTTGGCGCATGGTCGCTGATG 1080
     AspLeuTyrAspThrThrArgLeuGlyHisAspSerProValGlyAlaTrpSerLeuMet

1081 TCTTCCGGAAGCCATACAGGTAAGATCTTCCAAACCCAACCAACCGGATTTGATCCTTGG 1140
     SerSerGlySerHisThrGlyLysIlePheGlnThrGlnProThrGlyPheAspProTrp

1141 TCCAAAATGATGCTGCAGGAAATGTATGGGGGCAAGTGGATTGAGCCGCAAGTCATCAAT 1200
     SerLysMetMetLeuGlnGluMetTyrGlyGlyLysTrpIleGluProGlnValIleAsn

1201 TACGAAGACCTGAAAAAACGGAAAAAGCAGGCTTCGCTCTACGATGGCAGCAGCCTCGAT 1260
     TyrGluAspLeuLysLysArgLysLysGlnAlaSerLeuTyrAspGlySerSerLeuAsp

1261 GAAGATGGCAAAGTCATCAAGCTGAATATGCCGCAAGTAGAGAAGACACCGCCGGTTCAA 1320
     GluAspGlyLysValIleLysLeuAsnMetProGlnValGluLysThrProProValGln

1321 CCGAAAGACGGCGATTATTCTTACTTCTCCGATGAGGGCGACAATCTGAACACGAAGATG 1380
     ProLysAspGlyAspTyrSerTyrPheSerAspGluGlyAspAsnLeuAsnThrLysMet

1381 ACTTCGGAAGTGATCGACCTGACAGGCGCCAGCTCCGCATCGATGAGCTTCGACTCCTGG 1440
     ThrSerGluValIleAspLeuThrGlyAlaSerSerAlaSerMetSerPheAspSerTrp

1441 AGAGCGATCGAGACCGGGTACGACTACCTGTACGTGAACGTGATTGATGTCGACTCAGGT 1500
     ArgAlaIleGluThrGlyTyrAspTyrLeuTyrValAsnValIleAspValAspSerGly

1501 GAGAGCACAACAGTAAAAGAGTACGATGACGAAACCAAAGGCTGGGATAAGGAAGAAATC 1560
     GluSerThrThrValLysGluTyrAspAspGluThrLysGlyTrpAspLysGluGluIle

1561 AGCCTGAACGATTTCGCTGGCAAAAAGATTCAAGTCGAGTTCAACTACGTGACGGATGGC 1620
     SerLeuAsnAspPheAlaGlyLysLysIleGlnValGluPheAsnTyrValThrAspGly

1621 GGCTTGGCGATGTCCGGCTTCTATCTGGATAATTTTGCAGTCACAGCAGACGGCGAAGTA 1680
     GlyLeuAlaMetSerGlyPheTyrLeuAspAsnPheAlaValThrAlaAspGlyGluVal

1681 GTCTTCTCGGATGATGCAGAAGGCGACCAGAAGTTTGATCTGGATGGATTCATCCATTTC 1740
     ValPheSerAspAspAlaGluGlyAspGlnLysPheAspLeuAspGlyPheIleHisPhe
```

Fig. 11

```
1741  GACGGCGAAGGCAAAATGTACGACGCGTACTACCTGGTAGAGCTGCGCTCCCATGAAGGC  1800
      AspGlyGluGlyLysMetTyrAspAlaTyrTyrLeuValGluLeuArgSerHisGluGly

1801  GTGGACGAGGGTCTGAAATACTTCCGCCGCAATGACACATTCTTCACGTATGATCCAGGT  1860
      ValAspGluGlyLeuLysTyrPheArgArgAsnAspThrPhePheThrTyrAspProGly

1861  CTGGTGATCTGGTACTACGATGGACGCTTTGGCAAAACGCAAGACAACAACACCAGCAAC  1920
      LeuValIleTrpTyrTyrAspGlyArgPheGlyLysThrGlnAspAsnAsnThrSerAsn

1921  CATCCAGGCTACGGCATGCTGGGCGTAGTCGATGCGCATCAGGAAGTTCGTTACTGGAAT  1980
      HisProGlyTyrGlyMetLeuGlyValValAspAlaHisGlnGluValArgTyrTrpAsn

1981  AACGATGAGGGCAACGAGGAGGCCATTGCCGACTCCCGTTACCAAGTGAACGATGCGGCA  2040
      AsnAspGluGlyAsnGluGluAlaIleAlaAspSerArgTyrGlnValAsnAspAlaAla

2041  TTCAGCCCGAACAAAACCTCCGGCATGGATCTCGACTACATTCTCGGCACGATGGATTAC  2100
      PheSerProAsnLysThrSerGlyMetAspLeuAspTyrIleLeuGlyThrMetAspTyr

2101  GAGCCGCTGAAAGGCATTACCGTATTCAAAGACAGTGATGATTACACGATGCCGGAAGTT  2160
      GluProLeuLysGlyIleThrValPheLysAspSerAspAspTyrThrMetProGluVal

2161  CCGGAAATCGGAAAAATCCTGCCGAAGATCGGTCTGCAAATCAAATTAATTCGTGTGTCC  2220
      ProGluIleGlyLysIleLeuProLysIleGlyLeuGlnIleLysLeuIleArgValSer

2221  AAGAAATTCACGAACGCACAGGTCGAGTTCTCCATCAAAAAATAA  2265
      LysLysPheThrAsnAlaGlnValGluPheSerIleLysLys***
```

Fig. 12

imp

```
1   ATGAACCATCCTGATTTTCGCGATCTACCCGCCTGCATGGAAGACGTAACCCTCGCTGCC   60
    MetAsnHisProAspPheArgAspLeuProAlaCysMetGluAspValThrLeuAlaAla

61  CTGGACGAGTACACTGGTCCACCAGATCCGACCGAATACCAATCATTGTATGGACGCTTG  120
    LeuAspGluTyrThrGlyProProAspProThrGluTyrGlnSerLeuTyrGlyArgLeu

121 CAAGAGGTTGCCGAAACTCTCCCTCCGCTCTATCGGGAGCATGTGTATCACCCTTTTCTT  180
    GlnGluValAlaGluThrLeuProProLeuTyrArgGluHisValTyrHisProPheLeu

181 CAAGCGATGGACAAGTTGTCTGAGTCAGGATTTGCGCAGATGCTCCGTCGAGATCCTCAA  240
    GlnAlaMetAspLysLeuSerGluSerGlyPheAlaGlnMetLeuArgArgAspProGln

241 AAAGAGCGAGAAGCCGGTCTGTTTTGCGATATCGCACAGGCCATTCTGCAAAACGGCGAA  300
    LysGluArgGluAlaGlyLeuPheCysAspIleAlaGlnAlaIleLeuGlnAsnGlyGlu

301 GCGTATGAACGCGATGCCACGGATGCCTTTCAGGAAGTAGTCAGCGATTTGTACGACGGT  360
    AlaTyrGluArgAspAlaThrAspAlaPheGlnGluValValSerAspLeuTyrAspGly

361 TTTTTAAGCGAGGAAGACAGGAGTGGCATCAAACCGCCTGATGAAAGCTTGATTGCTCCT  420
    PheLeuSerGluGluAspArgSerGlyIleLysProProAspGluSerLeuIleAlaPro

421 CTGGTCAAATGGGGACGCCCGCAATTCGGACCTTATACGTGGACAGCTGAAGCCGCTGCC  480
    LeuValLysTrpGlyArgProGlnPheGlyProTyrThrTrpThrAlaGluAlaAlaAla

481 CATTTTGGCATCAAGACGGGCATTGTCAATTTGCCCCCGGCAAACGCCCGCCTGGGTCTG  540
    HisPheGlyIleLysThrGlyIleValAsnLeuProProAlaAsnAlaArgLeuGlyLeu

541 CTCGCGTGGTCTGCATTAGGTCACGAAACGGCTGGACACGACATTCTCCACGCCGACACC  600
    LeuAlaTrpSerAlaLeuGlyHisGluThrAlaGlyHisAspIleLeuHisAlaAspThr

601 GGTTTGCTTGGAGAACTGCAGCAAACCGTCTATGACGCTTTGTTTGATGAGCTTCACAAT  660
    GlyLeuLeuGlyGluLeuGlnGlnThrValTyrAspAlaLeuPheAspGluLeuHisAsn

661 CGGACGCTGGCGGACTACTGGTCGCTCCGAATCGACGAGACTGCCTCCGACGTTTTGGGA  720
    ArgThrLeuAlaAspTyrTrpSerLeuArgIleAspGluThrAlaSerAspValLeuGly

721 ATCCTGAACACCGGCCCCGCTGCAGGGATTGGACTGATTGGATATTTCCGCGGCCTTAAT  780
    IleLeuAsnThrGlyProAlaAlaGlyIleGlyLeuIleGlyTyrPheArgGlyLeuAsn

781 AAGGCGTACACCGGACAAGCAACACTGCGGAATACAGGGCCACAGAATGACCCACATCCA  840
    LysAlaTyrThrGlyGlnAlaThrLeuArgAsnThrGlyProGlnAsnAspProHisPro
```

Fig. 13

```
841  GCAGACATCTTGCGCGGTTATCTTGCTGCTGAGACTGCTCGTCTGCTGCATTTTGACAAC  900
     AlaAspIleLeuArgGlyTyrLeuAlaAlaGluThrAlaArgLeuLeuHisPheAspAsn

901  GCATCCGACTGGGCACAGGCACTTCTCGAGGAAACCAGGCGTGATCTTAAAGGCATCACA  960
     AlaSerAspTrpAlaGlnAlaLeuLeuGluGluThrArgArgAspLeuLysGlyIleThr

961  ATAGGCAGAGCCTCTTTGGATGCAGAAACCGCTCAAAAATCTGCTGCCATTGTCGCTCGC 1020
     IleGlyArgAlaSerLeuAspAlaGluThrAlaGlnLysSerAlaAlaIleValAlaArg

1021 ACAATTATGGAAGCACGCCTGCTCAGTCTGGAAGGTCATGCCCTCGGGCAAATTCAAAAC 1080
     ThrIleMetGluAlaArgLeuLeuSerLeuGluGlyHisAlaLeuGlyGlnIleGlnAsn

1081 TGGCACAACGAGGATGAACGAATCGTTCAGGAAATTCGCTCCCATTTTACAGGTTCCCTG 1140
     TrpHisAsnGluAspGluArgIleValGlnGluIleArgSerHisPheThrGlySerLeu

1141 ACCGTGCAAGACGGCATTGTTTCGGGTATGTATGCTGCGCATGTCGTGGCAGCAGCCGTC 1200
     ThrValGlnAspGlyIleValSerGlyMetTyrAlaAlaHisValValAlaAlaAlaVal

1201 CAAGCAGCCGTTTCAGGAGAGATGGATACCTCCGCTGCCTTCACAGGGATGAAAACCTTG 1260
     GlnAlaAlaValSerGlyGluMetAspThrSerAlaAlaPheThrGlyMetLysThrLeu

1261 CTGAAGAGCATGCACGACGCCAATCCTTCCTGGGGACCTCTCTATGTACGATATCGCGGT 1320
     LeuLysSerMetHisAspAlaAsnProSerTrpGlyProLeuTyrValArgTyrArgGly

1321 GATCTCACTCCGCATCGCATTTACTCCCGTTCTGCGAGCTAG  1362
     AspLeuThrProHisArgIleTyrSerArgSerAlaSer***
```

Fig.14

| PRIMER NAME | OLIGONUCLEOTIDE SEQUENCE |
|---|---|
| Hos P1 | gggggtacctcactctgtcagcatgctg |
| Hos P2 | gggggatcccggcgtgattcccactgc |
| Hos P3 | gggctgcagatagcggatgaaggtgtg |
| Hos P4 | gggtctagacctgcttatacatctgtttcg |

Fig.15

| PRIMER NAME | OLIGONUCLEOTIDE SEQUENCE |
|---|---|
| imp P1 | gagagaccATGGACCATCCTGATTTTCGCGATCTACCCG |
| imp P2 | agaattcagtggtggtggtggtggtggtggtgGCTCGCAGAACGGGAGTAAATGCGATGC |

Fig. 16

flp P1: aaaagaattctttctgcagaacaggatgcgggggagccgccgct

Fig. 17

flp P2: aaaaaggatccttatagcatctaatcttcaacaaact

Fig. 18

flp P3: aaaaaaagatcttgaacgatgacctctaataattgttaa

Fig. 19

flp P4: aaaagaattcaaatctagaaagtgtgtgctctgcgaggctgtc

Fig. 20

flp P5: tccatggcacaatttggtatattatgtaaa

Fig. 21

flp P6: actcgagttatatgcgtctatttatgtaggat

Fig. 22

flp P7. ttttttctagactttatgaatataaagtatagtgtgt

Fig. 23

flp P8: gggggctgcagttatatgcgtctatttatgtaggatg

Fig.24

| PRIMER NAME | AMINO ACID SEQUENCE DATA | PRIMER OLIGONUCLEOTIDE SEQUENCE |
|---|---|---|
| emp P1 | LysArgValHisThrAspAsnLeu | aaRcgIgtNcaYacNgaYaaYct |
| emp P2 | PheGlnThrGlnProThrGlyPhe | aaNccIgtNggYtgNgtYtggaa |

I : INOSINE, R : A or G, Y : C or T, N : A or G or T or C

Fig.25

| PRIMER NAME | OLIGONUCLEOTIDE SEQUENCE |
|---|---|
| emp P3 | cctcgtagtgcttttggtcgaag |
| emp P4 | accaataccggagtgaaccagca |
| ADAPTOR PRIMER | actatagggcacgcgtggt |

Fig. 26

ctcccatggctttcgctacccccgtgcagtccgtggactgc

Fig. 27

atataagcttttagggagagaggacttccatggt

Fig. 28

tttctgcaggtaaaatcgaagaaggtaaactggta

Fig. 29

aaaaagcttttacttggtgatacgagtctgcgcg

Fig. 30

ttttggatccgaggaggtgtcggagaactgtagccac

Fig. 31

aaaaagcttctacactggcagctcctcctgtctg

Fig. 32

aaggatccccgtcatatccggca

Fig. 33

aaaagctttaggcgttatccgctttagc

Fig. 34

tatatccatggcttcttactgccaggcgccctttttaa

Fig. 35

atataagcttttattttgatgctctctggccttggaa

Fig. 36

atattcatgagcaacgacttgcttcgatccca

Fig. 37

atataagctttcagttctggagataatctgtaagta